AMENDMENTS TO THE SPECIFICATION

Please replace the paragraphs beginning on page 12, line 1 and ending on line 17 with the following amended paragraphs:

Figure 2 (SEQ ID NOS: 86-114) shows a sequence alignment of DnaJ-like domains of plant and cyanobacterial Ftn2 proteins (indicated by asterisk) and DnaJ domains from Pfam database. Total about 270 DnaJ domains from the database were aligned with the ARC6 proteins. Shown in this figure are only selected DnaJ domains most similar to Ftn2 proteins. Black and gray columns indicate that identical or similar amino acid, respectively, was present in 70% of all aligned sequences at that position. The TrEMBL accession codes and location of the DnaJ domain within the protein are shown for the Pfam database records. For the ARC6 homologues, if the protein sequences were derived from EST records and did not encompass the initial M, the location of the DnaJ domain is not given.

Figure 3 (SEQ ID NOS:115-124) shows an alignment of plant and cyanobacterial Ftn2 full and partial sequences. Partial sequences are marked by asterisk (*). Not shown are the N-termini of the plant sequences, which contain chloroplast transit peptides. Light-gray and black columns indicate similarity and identity, respectively, greater than 80%. Gaps are indicated by a dash (-), missing sequence by an underline (_). Similarity and identity calculations do not include missing sequences. The Dna-J like domain is indicated by a solid line (▬). Putative myb domain is indicated by diamonds (♦). Site of truncation of the protein in *arc6* mutant is marked by a triangle (▲) at position 398 of the alignment (residue 325 of AtFtn2).

Please replace the paragraph beginning on page 13, line 15 and ending on line 21 with the following amended paragraph:

Figure 4 (SEQ ID NOS:195-197) shows an alignment of the AtARC5 gene with Dynamin-1 from *Homo sapiens* and Dnm1p from *Saccharomyces cerevisiae*. Gray boxes indicate completely conserved residues; yellow boxes are identical residues; cyan boxes are similar residues; dashes indicate gaps. The domain structure is indicated by the lines above the alignment. Red, GTPase domain; green, middle domain; blue, PH domain; lavender, GTPase effector domain; black, PR domain. The dotted underline indicates the sequence encoded by the

alternatively spliced intron in *ARC5*. The triangle indicates the position of the *arc5* mutation.

Please replace the paragraph beginning on page 40, line 24 and ending on page 41, line 3 with the following amended paragraph:

The product of the cyanobacterial *Ftn2* gene from *Synechococcus* sp. strain PCC 7942 was discovered to share a similarity with an unknown protein of *Arabidopsis thaliana* (AB016888|Q9FIG9; BLAST score, 72.8; Expect = 1 x 10^{-11}). It was therefore contemplated that this ortholog was involved in plastid division in Arabidopsis cells. The encoded product of this Arabidopsis *Ftn2* ortholog was predicted to posses a chloroplast transit peptide (from a web-based program (http://, followed by, HypothesisCreator.net/iPSORT/), with the amino acid sequence MEALS HVGIG LSPFQ LCRLP PATTK LRRSH (SEQ ID NO:28). The Arabidopsis protein was also predicted to possess a DnaJ domain profile according to ProfileScan (http://, followed by, www.isrec.isb-sib.ch/software/PFSCAN_form.html), and a Myb DNA-binding domain, according to InterProScan (http://, followed by, www.ebi.ac.uk/interpro/scan.html).

Please replace the paragraph beginning on page 108, line 4 and ending on line 14 with the following amended paragraph:

To determine whether the wild type *ARC5* gene could complement the mutation, the predicted *ARC5* gene (a transgene containing the predicted At3g19730 /At3g19720 locus plus 1.9 kb and 1.1 kb of the 5' and 3' flanking DNA, respectively) was amplified from the DNA of BAC MMB12 by PCR using the primers 5'- GGAATTCCGAGTCGAGTTGCTTTGTTG-3' (SEQ ID NO:78) and 5'- CGTCTAGAGCTTACCTCAAAGGTACATGGA-3' (SEQ ID NO:79). The PCR product was digested with *Eco*RI and ligated into a derivative of the transformation vector pLH7000 (http://www.dainet.de/baz/jb2000/jb_2000direkt.htm) digested with *Eco*RI and *Sma*I. The construct was transferred to *A. tumefaciens* GV3101 and introduced into *arc5* plants by floral dipping. The phenotypes of the T_1 plants were determined by microscopy. Microscopic analysis of T_1 transgenic plants indicated that the chloroplast division defect in the mutant was fully or partially rescued by the wild-type transgene.

On page 110, please replace the paragraph beginning on line 17 and ending on page 111, line 13 with the following amended paragraph:

The subcellular localization of ARC5 was investigated by expressing a GFP-ARC5 fusion protein in transgenic plants. The GFP sequence was amplified from plasmid smRS-GFP (Davis, S. J. & Vierstra, R. D. (1998) *Plant Mol. Biol.* 36, 521-528) with the primers 5'-CGGGATCCATGAGTAAAGGAGAAGAACT-3' (SEQ ID NO:80) and 5'-GCTCTAGATAGTTCATCCATGCCATGT-3' (SEQ ID NO:81). The PCR product was digested with *Bam*HI and *Xba*I. The *ARC5* coding region and 1.1 kb of the 3' flanking DNA were amplified from the MMB12 BAC clone with primers 5'-GGACTAGTACGATGGCGGAAGTATCAGC-3' (SEQ ID NO:82) and 5'-CGGGATCCGCACCGAAGGAGCCTTTAGATT-3' (SEQ ID NO:83). The PCR product was digested with *Spe*I and *Eco*RI. cDNA fragments encoding GFP and ARC5 were subcloned into Bluescript KS+ (Stratagene) that had been digested with *Eco*RI and *Bam*HI to create a *GFP-ARC5* fusion construct. The *ARC5* promoter was amplified from MMB12 with primers 5'-GACTAGTTGGCTCAACGCTTACCTCAA-3' (SEQ ID NO:84) and 5'-CGGGATCCGCCATCGTCTCTTACGA-3' (SEQ ID NO:85), and cloned into Bluescript KS+ (Stratagene) between the *Spe*I and *Bam*HI sites. The promoter fragment was then subcloned into the plasmid containing the *GFP-ARC5* fusion construct at the 5' end of the fusion. The resulting plasmid was digested with *Spe*I and *Eco*RI, and the promoter-*GFP-ARC5* cassette was subcloned into a derivative of the transformation vector pLH7000 (http://, followed by, www.dainet.de/baz/jb2000/jb_2000direkt.htm). The plasmid was transferred to *A. tumefaciens* GV3101 and used to transform wild-type *A. thaliana* plants (Col-0) as described above. The GFP-ARC5 localization pattern was visualized by fluorescence microscopy in T_1 plants. For *in vivo* detection of green fluorescent protein (GFP), fresh leaf tissue was mounted in water and viewed with an L5 filter set (excitation 455 nm to 495 nm, emission 512 to 575 nm) and a 100X oil immersion objective of a Leica DMR A2 microscope (Leica Microsystems, Wetzlar, Germany) equipped with epifluorescence illumination. Images were captured with a cooled CCD camera (Retiga 1350EX, Qimaging, Burnaby, British Columbia, Canada) and processed with Adobe Photoshop imaging software (Adobe Systems, San Jose, CA).